Quantitative genetic analysis of the metabolism of key fermentation aroma by wine yeast

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Quantitative genetic analysis of the metabolism of key aroma compounds by Saccharomyces cerevisiae during wine fermentation

Steyer D 1,2,3, Ambroset C 4,5,6, Brion C4,5,6, Claudel P1,2, Delobel P4,5,6, Sanchez I4,5,6, Erny C7, Blondin B4,5,6, Karst F1,2, Legras JL 4,5,6

Introduction

Wine aromatic profile is the combination of vine aromatic compounds that can be metabolized by yeast and of compounds produced by yeast during alcoholic fermentation. The variability of the influence of wine yeast strains on wine aroma is well known from wine makers who have selected numerous strains produced nowadays at an industrial scale. Even though several genes involved in the production of aroma have already been described, little is known about the genetic basis of the variability of the metabolism of these compounds. In order to answer this issue, we compared the aroma production and the geraniol metabolism during alcoholic fermentation using a progeny of 30 strains. This progeny was obtained from a cross between *S. cerevisiae* strains S288C and 59A, and was previously mapped using oligonucleotide microarrays.

Methods

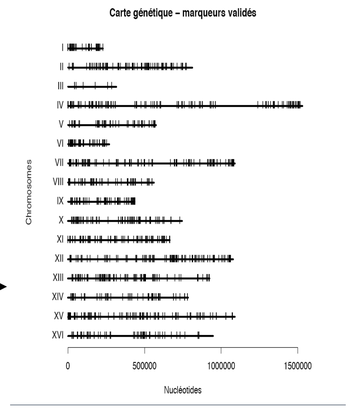
Strains :

Haploid derivative from EC1118 : 59a × Lab strain S288c

Test for fermentation abilities

about 60 segregants → 30 segregants

CGH characterization : high density genetic map with 1900 validated markers



30 strains

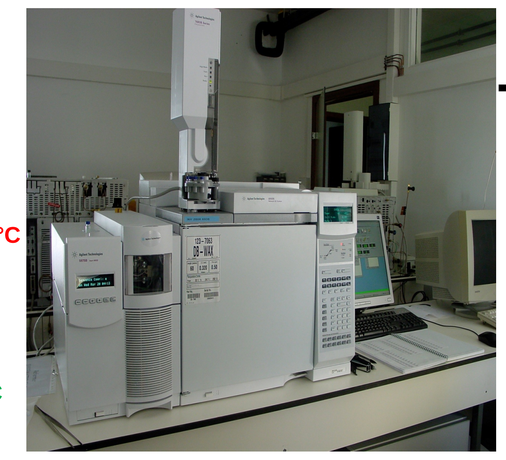
Alcoholic fermentation of a synthetic medium that mimics grape juice, spiked with or without of geraniol

Medium A : 1mg/L geraniol
1% Anaerobical factor 1L, 20°C

Medium B : 5mg/L geraniol
1% Anaerobical factor 250mL, 20°C

Medium C : 0mg/L geraniol
100% Anaerobical factor 1L, 28°C

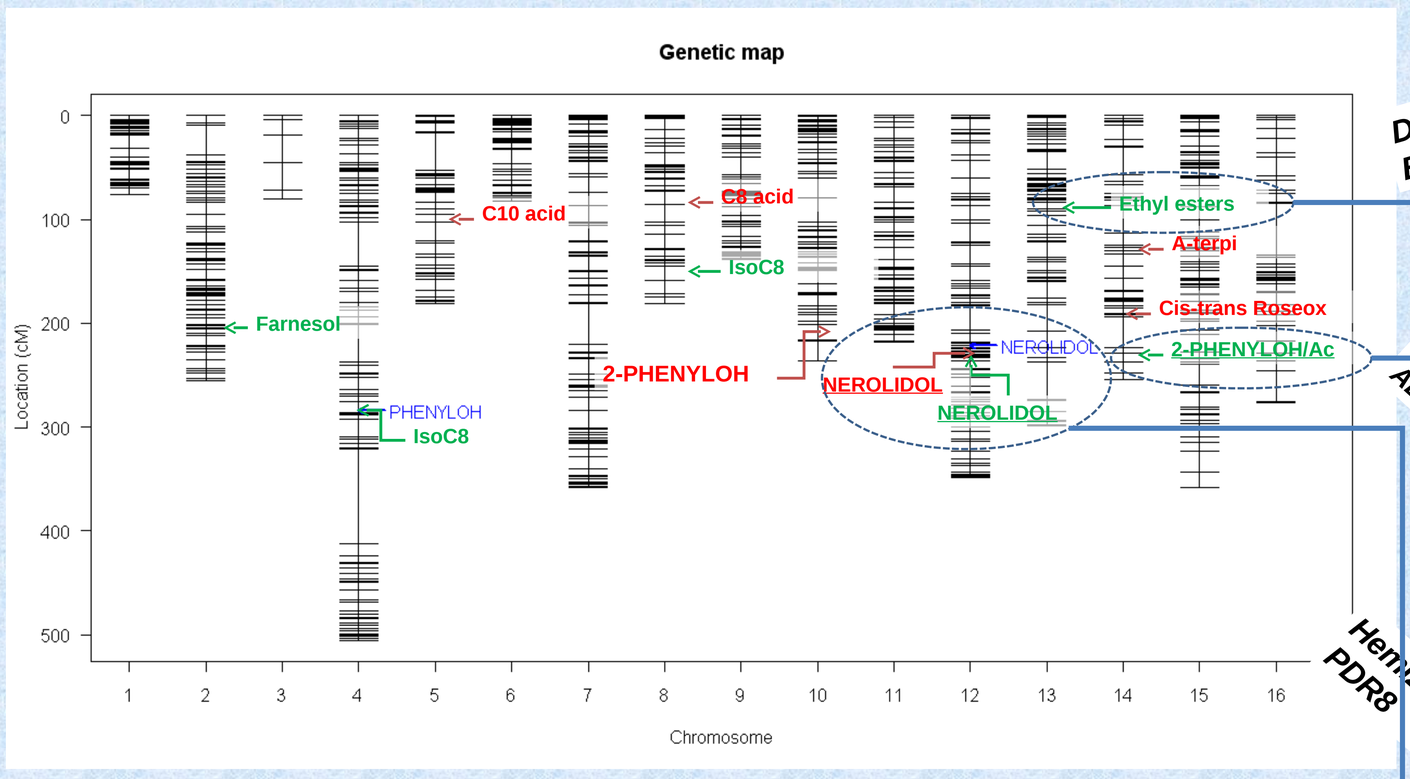
SBSE -LD extraction of aromatic compounds



QTL analysis with R/QTL and J/QTL

Candidate gene + validation

Results/conclusion



mQTL detected with J/QTL and R/QTL => LOD score > 3 ; p-value < 0,05 ; in blue QTL obtained with medium A ; in red QTL obtained with medium B ; in gree QTL obtained withe medium C

Ethyl octanoate (fruity)

Ethyl decanoate (fruity)

DeletionPLB1/PLB2

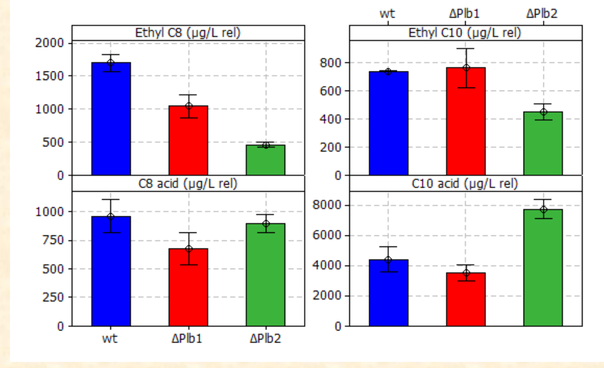


Fig 1 : effect of the deletion of PLB1/PLB2 ont ethyl esters and medium chain fatty acids concentration in enological condition(BY background)

Hemizigote comparison ABZ1

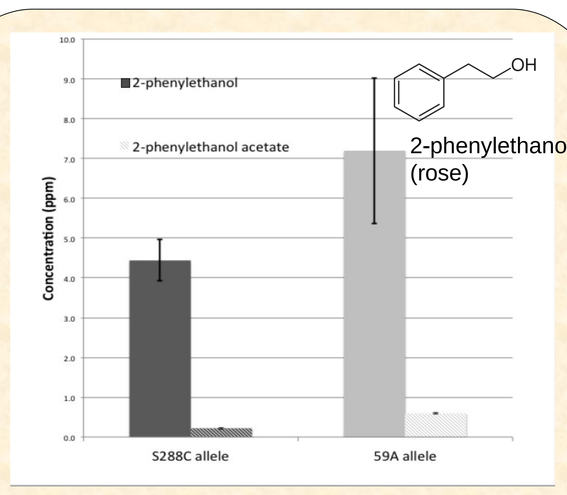


Fig 2 : effect of the allelic expression of ABZ1 in enological condition on 2-phenylethanol/acetate concentration

Hemizigote comparison PDR8

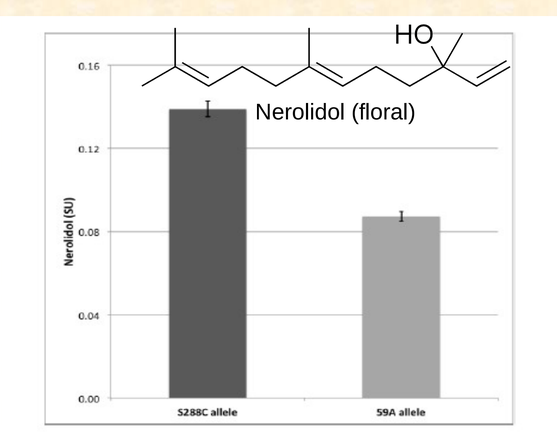


Fig 3 : Effect of the allelic expression of PDR8 in enological condition on nerolidol concentration

We detected 13 mQTL involved in the production of volatile compounds by yeast during fermentation. One was investigated by deletion and two by hemizigote comparison.
In a “By” background, deletion of Phospholipase B2 gene (*PLB2)* reduces drastically the concentration of ethyl octanoate and decanoate and increases the concentration of decanoic acid **(fig 1)**. In the same condition, deletion of its homolog *PLB1* contributes only to a decrease of ethyl octanoate **(fig 1).**
Thanks to hemizigote we show that the allelic version of the Para-aminobenzoate synthase (*ABZ1)* is involved in the production of 2-phenyl –ethanol/-acetate (rose/honey) **(fig 2)**.
We also demonstrate that the alleles of the transcription factor P*DR8* found S288C and 59A differently regulate the release of nerolidol into the media **(fig 3)** (target : *QDR2* data not shown).

This study illustrates the value of QTL analysis for the analysis of metabolic traits, and in particular the production of wine aromas. It also identifies the particular role of the *PDR8* gene in the production of farnesyldiphosphate derivatives, of *ABZ1* in the production of numerous compounds and of *PLB2* in ethyl ester synthesis. This work also provides a basis for elucidating the metabolism of various grape compounds, such as citronellol and cis-rose oxide.

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**Wikipedia*